

**FIGURE 1A**  
**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L W V L L L W V P G S T G D I V M T Q S P D S L
<-----Leader-----> <-----FR1----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
<-----> <-----CDR1-----> <----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S T
<-----FR2-----> <-----CDR2-----> <-----FR3----->
GAC TTC ACC CTC ACC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
<-----> <-----CDR3-----> <----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CCA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
<-----FR4-----> <-----Constant----->
GTT GTG TGC CTG ATC AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
<----->
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG AGC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
<----->
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
<----->
```

**FIGURE 1B**  
**TRX1 Light Chain Nucleic Acid Sequence**

ATGAGACAGACAAATCCTGCTATGGGTGCTGCTGCTCTGGGTCCAGGCTCCACTGGTGACAT  
TGTGATGACCCAAATCTCCAGATTCTTTGGCTGTGCTCTAGGTGAGAGGGCCACCATCAACTGCAAG  
GCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAAGTGGTATCAACAGAAACCCAGGACAG  
CCACCCAAACTCCTCATCTATGTTGCATCCAAATCTAGAGTCTGGGTCCCAGACAGGTTTAGTGG  
CAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGCGGAGGATGTTGCAGTCT  
ATTACTGTCAGCAAAAGTCTTCAGGACCCCTCCGACGTTTCGGTGGAGGTACCAAGGTGGAAATCAA  
CGAACTGTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACT  
GCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGAT  
AACGCCCTCCAAATCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTA  
CAGCCTCAGCACACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCG  
AAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG

**FIGURE 1C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDTILLWVLLWVPGSTGDI VMTQSPDLSAVSLGERATIN**CKASQSV**DYDGD**SYMNWY**QQKPG  
QPPKLLI**YVASNLE**SGVPDRFSGSGGTDFTLTISSLQAEDVAVY**CCQSLQDPP**TFGGGTKVEIKR  
TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS  
SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDLSAVSLGERATIN**CKASQSV**DYDGD**SYMNWY**QQKPGQPPKLLI**YVASNLE**SGVPDR  
FSGSGGTDFTLTISSLQAEDVAVY**CCQSLQDPP**TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT  
ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEV  
THQGLSPVTKSFNRGEC

**FIGURE 1D**  
**TRX1 Heavy Chain**

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GTC TAT GTC ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
<-----FR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTC ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S Y Y N E K F K G R V T M T R D T
<-----CDR2----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
<-----FR3----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
<-----FR4----->
TCT GGG GGC ACA GCG GCC CTG TGC TGC ATG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
<-----Constant----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T
<----->
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
<----->
TGC CCA GCA CCT GAA CTC GCG GGG GCA CCG TCA GTC TTC CTC TCC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CCG ACC CCT GAG GTC
C P A P E L A G A P S V F L F P P K P K D T L M I S R T P E V
<----->
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
<----->
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App No.: Not Yet Assigned

Docket No.: TLN-022

Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

CCG CGG GAG GAG CAG TAC AAC AGC AGC TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S

AAT GGG CAG CCG GAG AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P

GGT AAA TGA  
G K \*  
----->

**FIGURE 1E**  
**TRX1 Heavy Chain Nucleic Acid Sequence**

ATGGAATGGATCTGGATCTTCTCCTCATCCTGTCTCAGGAACCTCGAGGTGTCCAGTCCCAGGTTCCAGCTGGTGCA  
GTCTGGAGCTGAAGTGAAGACCTGGGGCTTCAGTGAAGGTGTCCTGTAAAGCTTCTGGATACACATTCACCT  
GCCATGTTATAAGCTGGTGAGGCAGGCACCTGGACAGGGCCTTGAGTGGATGGGAGAGATTTATCCTGGAA  
GGGTAGTAGTTATTATATGAGAAAGTTCAAGGCAGGGTCACAATGACTAGAGACACATCCACGACGACAGTC  
TACATGGAACCTCAGCAGCCTGAGGTCTGAGGACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTC  
GGTTGTTTACTGGGCCAAGGGACACTAGTCACAGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC  
CCTGGCACCTCCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC  
CGAACCGGTGACGGTGTGCGTGAACCTCAGCGCCCTGACACAGCGGTGCACACCTTCCCCTGCTCCTACA  
GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC  
TGCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGTGACAAACTCA  
CACATGCCACCGTGCCAGCACCTGAACCTCGCGGGCACCGTCAAGTCTTCTTCCCCTCCAAACCCCAAG  
GACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAAGACCCCTGAG  
GTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGTCAGCGTCTCACCGTCTGCACCAAGACTGGCTGAATGGCAAGGAGTACAAGT  
GCAAGGTCTCCAACAAAGCCCTCCAGCCCTCATCGAAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAG  
AACCACAGGTGTACACCCCTGCCCTCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCCCTGG  
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGA  
CCACGCTCCCGTGTGACTCCGACGGCTCCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTG  
GCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAGAGCCTC  
TCCCTGTCTCCGGGTAAATGA

**FIGURE 1F**  
**TRX1 Heavy Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

MEWIWIFLLILSGTRGVQSQVLVQSGAEVKPGASVKVCKASGYTFT**AYVISWVRQAPGQGLEW**  
**MGEIYPGSGSSYYNEKFKGR**VTMTTRDTSTSTVYMELSSLRSEDTAVYCAR**SGDGSRFVYWGQG**  
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG  
LYSLSSVWTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMIS  
RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKA  
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

**Without leader sequence:**

QVQLVQSGAEVKPGASVKVCKASGYTFT**AYVISWVRQAPGQGLEWMGEIYPGSGSSYYNEKF**  
**KGR**VTMTTRDTSTSTVYMELSSLRSEDTAVYCAR**SGDGSRFVYWGQ**GLTVTVSSASTKGPSVFPLA  
PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM  
HEALHNHYTQKSLSLSPGK

**FIGURE 2A**

**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L L W V L L L W V P G S T G D I V M T Q S P D S L
-----Leader----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA ACT GTT GAT TAT GAT GCT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
-----CDR1----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S G T
-----PR2----->
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
-----CDR3----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CTA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A L S V F I F P P S D E Q L K S G T A S
-----PR4----->
GTT GTG TGC CTG ATC AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
-----
GTC ACA GAG CAG GAC AGC AAC GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L T L S K A D Y E K H K V Y A
-----
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
----->
```



**FIGURE 2B**

**TRX1 Light Chain Nucleic Acid Sequence**

ATGGAGACAGACAAATCCTGCTATGGTGCTGCTGCTCTGGGTTCCAGGCT  
CCACTGGTGACATTGTGATGACCCAATCTCCAGATTCTTTGGCTGTGCTCTA  
GGTGAGAGGGCCACCATCAACTGCAAGGCCAGCCAAAGTGTGATTATGATG  
GTGATAGTTATATGAACTGGTATCAACAGAAACCAGGACAGCCACCCAAACT  
CCTCATCTATGTTGCATCCAATCTAGAGTCTGGGTCCTCCAGACAGGTTTAGT  
GGCAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGGCGG  
AGGATGTTGCAGTCTATTACTGTCAGCAAAGTCTTCAGGACCCCTCCGACGTT  
CGGTGGAGGTACCAAGGTGGAAATCAAAACGAACCTGTGGCTGCACATCTGTC  
TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGT  
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG  
GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC  
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCA  
GACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGA  
GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

## **FIGURE 2C**

### **TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

METDTILLWVLLLVVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPGQPPK  
LLIYVASNLESGVPDRFSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKRTVAALS VFIF  
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYSLSTLTLSKADYEKH  
KVYACEVTHQGLSSPVTKSFNRGEC

Without leader sequence:

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPGQPPKLLIYVASNLESGVPDRFSGSG  
SGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKRTVAALS VFIFPPSDEQLKSGTASVVCLLNN  
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF  
NRGEC

**FIGURE 2D**

**TRX1 Heavy Chain  
(aglycosyl)**

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA CTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader-----> <-----PR1----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----PR2-----> <-----CDR1-----> <-----PR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTG ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
-----CDR2-----> <-----PR3-----> <-----CDR3----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----PR4-----> <-----Constant----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----PR4-----> <-----Constant----->
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG AAG GAC TAC TTC CCC GAA CCG GTG AGC GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----PR4-----> <-----Constant----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S L G T Q T
-----PR4-----> <-----Constant----->
TAT ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----PR4-----> <-----Constant----->
TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTG
C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V
-----PR4-----> <-----Constant----->
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
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Inventor: Dawn Windsor-Hines et al.  
Title: INDUCING TOLERANCE IN PRIMATES

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CCG CGG GAG GAG CAG TAC GCC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y A S T Y R V V S V L T V L H Q D W L N G K E Y K C

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S

AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GGC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P

GGT AAA TGA  
G K \*  
----->

FIGURE 2E

TRX1 aglycosyl mut Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTGTCAGGAACTCGAGGTGTCCAGTCCCAGGTTCA  
GCTGGTGAGTCTGGAGCTGAAGTGAAGAACCTGGGGCTTCAGTGAAGGTGTCCTGTAAAGGCT  
TCTGGATACACATTCACTGCCTATGTTATAAGCTGGGTGAGGCAGGCACCTGGACAGGGCCTTGA  
GTGGATGGGAGAGATTTATCCTGGAAAGCGGTAGTAGTTATTATAATGAGAAGTTCAAGGCGAGGG  
TCACAACTGACTAGAGACACATCCACCAGCACAGTCTACATGGAACCTCAGCAGCCTGAGGTCTGAG  
GACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTCGGTTTGTTTACTGGGGCCAAAG  
GGACACTAGTCACAGTCTCCTCAGCCTCCACCAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCC  
TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTGCTCAAGGACTACTTCCCCCGAAC  
CGGTGACGGTGTGCGTGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCCT  
ACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  
AGACCTACATCTGCAACGTGAATCACAAAGCCCCAGCAACACCAAGGTGGACAAGAAATTGAGCCC  
AAATCTTGTGACAAAACTCACACATGCCACCGTGCCCGAGCACCTGAACTCCTGGGGGACCGTC  
AGTCTTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATG  
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG  
GAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACGCCAGCACGTACCGTGTGTGTC  
GCGTCTCACCGTCTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA  
CAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAC

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AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCT  
GGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCCGGAGAAC  
AACTACAAGACCACGCCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCAC  
CGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTG  
CACAACCACTACACGCAGAGAGCCTCTCCCTGTCTCCGGGTAATGA

**FIGURE 2F**

**TRX1 Heavy Chain aglycosyl mut Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

MEWIIFLLILSGTRGVQSVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSY  
YNEKFKGRVTMTSDTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLTVTVSSASTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK  
VEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR  
EEQYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVK  
GFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Without leader sequence:

QVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSYNEKFKGRVTMTSDTST  
VYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV  
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE  
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ  
DWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  
NYKTTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

**FIGURE 3A**  
**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L L W V L L L W V P G S T G D I V M T Q S P D S L
<-----Leader----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
<-----CDR1----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S G T
<-----FR2----->
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
<-----CDR2----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CTA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A L S V F I F P P S D E Q L K S G T A S
<-----FR4----->
GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
<-----Constant----->
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
<----->
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
<----->
```



**FIGURE 3B**  
**TRX1 Light Chain Nucleic Acid Sequence**

[illegible]

**FIGURE 3C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDTILLWVLLWVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPG  
QPPKLLIYVASNLESGVPDRFSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKR  
TVAALSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL  
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPGQPPKLLIYVASNLESGVPDR  
FSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKRTVAALSVFIFPPSDEQLKSGT  
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLSTLTLSKADYEKHKVYACEV  
THQGLSSPVTKSFNRGEC

FIGURE 3D  
TRX1 Heavy Chain

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
-----Leader-----
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----FR1-----
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTG ACA ATG ACT AGA GAC ACA
-----CDR2-----
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----FR3-----
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----FR4-----
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----
GTG CAC ACC TTC CCG GCT CTC CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T
-----
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAT GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----
TGC CCA GCA CCT GAA CTC GCG GGG GCA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTG
C P A P E L A G A P S V F L F P P K P K D T L M I S R T P E V
-----
ACA TGC GTG GTG GAC GTG ACC CAC GAA GAC CCT GAG GTG AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
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App No.: Not Yet Assigned

Docket No.: TLN-022

Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C  
-----

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P  
-----

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S  
-----

AAT GGG CAG CCG GAG AAC TAC AAG ACC ACG CCT CCG GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F L Y S K L T V D K  
-----

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P  
-----

GGT AAA TGA  
G K \*  
----->

FIGURE 3E  
TRX1 Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTGTCAGGAATCGAGGTGTCCAGTCC  
CAGGTTCAGCTGGTGCAGTCTGGAGCTGAAGTGAAGAAGCCTGGGGCTTCAGTGA  
AGGTGTCCTGTAAAGCTTCTGGATACACATTCACCTGCCTATGTTATAAGCTGGGTGA  
GGCAGGCACCTGGACAGGGCCTTGAGTGGATGGAGAGATTTATCCTGGAAGCGG  
TAGTAGTTATTATAATGAGAAAGTTCAAGGGCAGGGTCACAATGACTAGAGACACATC  
CACCAGCACAGTCTACATGGAATCAGCAGCCTGAGGTCTGAGGACACTGCGGTCT  
ATTACTGTGCAAGATCCGGGGACGGCAGTCGGTTTGTTTACTGGGGCCCAAGGGACA  
CTAGTCACAGTCTCCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACC  
CTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC  
TACTTCCCCGAACCGGTGACGGTGTCTGTGGAATCAGGCGCCCTGACCAGCGGCG  
TGACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTG  
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA  
CAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAA  
CTCACACATGCCCACCGTGCCCCAGCACCTGAATCGCGGGGCGCACCGTCAGTCTT  
CCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA  
CATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTA  
CGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGGTCAAGCGTCTCACCGTCTCTGCACCAGGACTGGCTGA

.App No.: Not Yet Assigned

Docket No.: TLN-022

Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

ATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCATCGAG  
AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCC  
CCCATCCCCGGGATGAGCTGACCCAAGAACCAAGGTCAAGCCTGACCTGCCCTGGTCAAA  
GGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCAGCCGGAGA  
ACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCCCTCTAC  
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT  
CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCCTCTCCCTGTCT  
CCGGGTAAATGA

**FIGURE 3F**  
**TRX1 Heavy Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

MEWIFLLILSGTRGVQSQVLVQSGAEVKKPGASVKVSKASGYTFT**AYVISWVRQAPGQG**LEW  
MGEI**YPGSGSSYYNEKFKGRVT**MTTRDTSTSTVYMESSLRSEDTAVYCAR**SGDGS**RFVYWGQ  
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG  
LYSLSSVWTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMIS  
RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA  
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

**Without leader sequence:**

QVQLVQSGAEVKKPGASVKVSKASGYTFT**AYVISWVRQAPGQG**LEWMGEI**YPGSGSSYYNEKF**  
**KGRVT**MTTRDTSTSTVYMESSLRSEDTAVYCAR**SGDGS**RFVYWGQGTLLTVSSASTKGPSVFPLA  
PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM  
HEALHNHYTQKSLSLSPGK

**FIGURE 4A**  
**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L W V L L L W V P G S T G D I V M T Q S P D S L
<-----Leader-----> <-----FR1----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
<-----> <-----CDR1----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S T
<-----FR2-----> <-----CDR2----->
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
<-----> <-----CDR3----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CCA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
<-----FR4-----> <-----Constant----->
GTT GTG TGC CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
<----->
GTC ACA GAG CAG GAG AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
<----->
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
<----->
```



**FIGURE 4B**  
**TRX1 Light Chain Nucleic Acid Sequence**

ATGGAGACAGACAAATCCTGCTATGGGTGCTGCTGCTCTGGGTTCCAGGCTCCACTGGTGACAT  
TGTGATGACCCAAATCTCCAGATTCTTTGGCTGTCTCTAGGTGAGAGGCCACCATCAACTGCAAG  
GCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAACCTGATCAACAGAAACCCAGGACAG  
CCACCCAAACTCCTCATCTATGTTGCATCCAAATCTAGAGTCTGGGGTCCCAGACAGGTTTAGTGG  
CAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGGGCGGAGGATGTTGCAGTCT  
ATTACTGTCAGCAAAGTCTTCAGGACCCCTCCGACGTTTCGGTGGAGGTACCAAGGTGGAAATCAAA  
CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC  
GCCTCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGAT  
AACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTA  
CAGCCTCAGCACACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGG  
AAGTCACCCATCAGGGCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTTAG

**FIGURE 4C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDTILLWVLLWVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPG  
QPPKLLIYVASNLESGVPDRFSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPTFGGGTKVEIKR  
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL  
SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPGQPPKLLIYVASNLESGVPDR  
FSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT  
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLSTLTLSKADYEKHKVYACEV  
THQGLSPVTKSFNRGEC

**FIGURE 4D**

**TRX1 Heavy Chain  
(aglycosyl)**

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC TGA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader-----> <-----FRI----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----CDR1-----> <-----FR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTC ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
-----CDR2-----> <-----FR3----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----FR3-----> <-----CDR3----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----FR4-----> <-----Constant----->
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GGC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----> <----->-----> <----->----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S L G T Q T
-----> <----->-----> <----->----->
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----> <----->-----> <----->----->
TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC
C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V
-----> <----->-----> <----->----->
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
```

-----

CCG CGG GAG GAG CAG TAC GCC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAG TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y A S T Y R V V S V L T V L H Q D W L N G K E Y K C

-----

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P

-----

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S

-----

AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCG GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K

-----

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P

-----

GGT AAA TGA  
G K \*  
----->

**FIGURE 4E**

TRX1 aglycosyl mut Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTCAGGAACTCGAGGTGTCCAGTCCCAGGTTCA  
GCTGGTGCAGTCTGGAGCTGAAGTGAAGAAGCCTGGGGCTTCAGTGAAGGTGTCCTGTAAGGCT  
TCTGGATACACATTCACTGCCTATGTTATAAGCTGGGTGAGGCAGGCACCTGGACAGGGCCTTGA  
GTGGATGGGAGAGATTTATCCTGGAAGCGGTAGTAGTTATTATAATGAGAAAGTTCAAGGGCAGGG  
TCACAAATGACTAGAGACACATCCACCAGCACAGTCTACATGGAACCTCAGCAGCCTGAGGTCTGAG  
GACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTCGGTTTGTACTGGGGCCAAAG  
GGACACTAGTCACAGTCTCCTCAGCCTCCACCAGGGCCCCATCGGTCTTCCCCCTGGCACCCCTC  
CTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCCTGCTCAAGGACTACTTCCCCCGAA  
CCGGTGACGGTGTGCGTGAAGTCAAGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTC  
CTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA  
CCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG  
CCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCCAGCACCTGAACCTCCTGGGGGAC  
CGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC  
ACATGCGTGGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGACG  
GCGTGAGGTGCATAATGCCAAGACAAAAGCCGCGGAGGAGCAGTACGCCAGCACGTACCCGTG  
TGGTCAGCGTCCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGT  
CTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCCGA  
GAACCACAGGTGTACACCCCTGCCCCCATCCCCGGGATGAGCTGACCAAGAACCAGGTACGCCCTGA

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CCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  
GGAGAACTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCA  
AGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAGAGCCTCTCCCTGTCTCCGGGTAATGA

## **FIGURE 4F**

### **TRX1 Heavy Chain aglycosyl mut Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

MEWIWIFLLILSGTRGVQSQVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEI  
YPGSGSSYYNEKFKGRVTMTTRDTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLVTVSSAS  
TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSS  
LGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGSPSVFLFPPKPKDITLMISRTPEVTCVVV  
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE  
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFF  
LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Without leader sequence:

QVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSYYNEKFKGRVT  
MTRDTSTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV  
DKKVEPKSCDKTHTCPPCPAPELLGSPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV  
EVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP  
SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS  
CSVMHEALHNHYTQKSLSLSPGK

# FIGURE 5 HEAVY CHAIN

Sequence Range: 1 to 1356

10	20	30	40	50	60
CAG GTT CAA TTG GTG GAG TCT GGA GGC GTT GTA CAG CCT GGA AGG TCC CTG AGA CTC					
Q V Q L V E S G G G V V Q P G R S L R L>					
70	80	90	100	110	120
TCA TGT GCA GCT TCT GGA TTC ACT TTC AGT GAC TTT GGC ATG AAC TGG GTT CGA CAG GCT					
S C A A S G F T F S D F G M N W V R Q A>					
130	140	150	160	170	180
CCC GGG AAG GGG CTG GAA TGG GTG GCA CTG ATT TAC TAT GAT GGT AGT AAC AAG TTC TAT					
P G K G L E W V A L I Y Y D G S N K F Y>					
190	200	210	220	230	240
GCA GAC TCT GTG AAG GGT CGA TTC ACC ATC TCC AGG GAC AAT TCT AAG AAC ACC CTA TAC					
A D S V K G R F T I S R D N S K N T L Y>					
250	260	270	280	290	300
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACA GCC GTG TAT TAC TGT GCA AAA CCC CAC					
L Q M N S L R A E D T A V Y Y C A K P H>					
310	320	330	340	350	360
TAT GAT GGT TAT TAT CAC TTC TTT GAT TCC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC					
Y D G Y Y H F F D S W G Q G T L V T V S>					
370	380	390	400	410	420
TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC AAG AGC ACC TCT					
S A S T K G P S V F P L A P S S K S T S>					
430	440	450	460	470	480
GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG					
G G T A A L G C L V K D Y F P E P V T V>					
490	500	510	520	530	540
TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GGT GTC CTA CAG TCC					
S W N S G A L T T S G V H T F P A V L Q S>					



550                    560                    570                    580                    590                    600  
TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG  
S G L Y S L S S V V T V P P S S S L G T Q>

610                    620                    630                    640                    650                    660  
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG  
T Y I C N V N H K P S N T K V D K K V E>

670                    680                    690                    700                    710                    720  
CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG  
P K S C D K T H T C P P C P A P E L L G>

730                    740                    750                    760                    770                    780  
GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC  
G P S V F L F P P K P P K D T L M I S R T>

790                    800                    810                    820                    830                    840  
CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC  
P E V T C V V V D V S H E D P E V K F N>

850                    860                    870                    880                    890                    900  
TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC  
W Y V D G V E V H N A K T K P R E E Q Y>

910                    920                    930                    940                    950                    960  
AAC AGC ACG TAC CGT GTG GTC AGC GTG CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC  
N S T Y R V V S V L T V L H Q D W L N G>

970                    980                    990                    1000                    1010                    1020  
AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC  
K E Y K C K V S N K A L P A P I E K T I>

1030                    1040                    1050                    1060                    1070                    1080  
TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT  
S K A K G G Q P R E P Q V Y T L P P S R D>

1090                    1100                    1110                    1120                    1130                    1140  
GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC  
E L T K N Q V S L T C L V K G F Y P S D>

1150                    1160                    1170                    1180                    1190                    1200

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ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC
I  A  V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P>

1210      1220      1230      1240      1250      1260
GTG CTG GAC TCC GAC GGC TCC TTC TTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG
V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R>

1270      1280      1290      1300      1310      1320
TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC
W  Q  Q  G  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y>

1330      1340      1350
ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
T  Q  K  S  L  S  L  S  P  G  K  *>
```

## FIGURE 6

## LIGHT CHAIN

Sequence Range: 1 to 648

			10			20			30			40				
GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	
D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G>	
50			60			70			80			90				
GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAA	GGA	AGT	CAG	GAT	ATT	AAC	AAT	TAC	
D	R	V	T	I	T	C	K	G	S	Q	D	I	N	N	Y>	
	100			110		120			130			140				
TTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	CTG	CTG	ATC	
L	A	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I>	
	150			160		170			180			190				
TAC	AAT	ACA	GAC	ATT	TTG	CAC	ACG	GGT	GTG	CCA	AGC	AGA	TTC	AGC	GGT	
Y	N	T	D	I	L	H	T	G	V	P	S	R	F	S	G>	
	200			210		220			230			240				
AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	CTC	CAG	CCA	
S	G	S	G	T	D	F	T	F	T	I	S	S	L	Q	P>	
	250			260		270			280							
GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	TAT	CAG	TAT	AAC	AAC	GGG	TAC	ACG	
E	D	I	A	T	Y	Y	C	Y	Q	Y	N	N	G	Y	T>	
290			300			310			320			330				
TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGA	ACT	GTG	GCT	GCA	CCA	
F	G	Q	G	T	K	V	E	I	K	R	T	V	A	A	P>	
	340			350		360			370			380				
TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	CAG	TTG	AAA	TCT	GGA	ACT	
S	V	F	I	F	P	P	S	D	E	Q	L	K	S	G	T>	
	390			400		410			420			430				
GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC	AGA	GAG	GCC	AAA	
A	S	V	V	C	L	L	N	N	F	Y	P	R	E	A	K>	
	440			450		460			470			480				
GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	
V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E>	

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      490      500      510      520
AGT  GTC  ACA  GAG  CAG  GAC  AGC  AAG  GAC  AGC  ACC  TAC  AGC  CTC  AGC  AGC
S    V    T    E    Q    D    S    K    D    S    T    Y    S    L    S    S>

530      540      550      560      570
ACC  CTG  ACG  CTG  AGC  AAA  GCA  GAC  TAC  GAG  AAA  CAC  AAA  GTC  TAC  GCC
T    L    T    L    S    K    A    D    Y    E    K    H    K    V    Y    A>

      580      590      600      610      620
TGC  GAA  GTC  ACC  CAT  CAG  GGC  CTG  AGC  TCG  CCC  GTC  ACA  AAG  AGC  TTC
C    E    V    T    H    Q    G    L    S    S    P    V    T    K    S    F>

      630      640
AAC  AGG  GGA  GAG  TGT  TAG
N    R    G    E    C    *
```